In the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

Claims 1–31. (Canceled)

32. (Previously Presented) An isolated polynucleotide fragment comprising a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, wherein said polypeptide shares at least 95% homology with SEQ ID NO:44 as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin.

33. (Previously Presented) The polynucleotide fragment of claim 32, wherein said polynucleotide comprises the coding region, nucleotides 594 to 2198, of SEQ ID NO:43.

34. (Previously Presented) The polynucleotide fragment of claim 32, wherein said polynucleotide is as set forth in SEQ ID NO:43.

35. (Previously Presented) The polynucleotide fragment of claim 32, wherein said polynucleotide sequence includes a segment of SEQ ID NO:43, said segment encodes said polypeptide having said heparanase catalytic activity.

36. (Previously Presented) The polynucleotide fragment of claim 32, wherein said polypeptide includes an amino acid sequence as set forth in SEQ ID NO:44.

37. (Previously Presented) The polynucleotide fragment of claim 32, wherein said polypeptide includes a segment of SEQ ID NO:44 said segment harbors said heparanase catalytic activity.

38. (Previously Presented) The polynucleotide fragment of claim 32, wherein said polynucleotide sequence is selected from the group consisting of double stranded DNA, single stranded DNA and RNA.

39. (Previously Presented) An isolated polynucleotide sequence as set forth in SEQ ID NO:43.

40. (Previously Presented) An isolated polynucleotide sequence at least 95% homologous to nucleotides 594 to 2198 of SEQ ID NO:43, as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin, wherein said polynucleotide sequence encodes a polypeptide having heparanase catalytic activity.

41. (Previously Presented) A vector comprising an isolated polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, wherein said polypeptide shares 95% homology with SEQ ID NO:44 as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin.

42. (Previously Presented) The vector of claim 41, wherein said polynucleotide comprises the coding region, nucleotides 594 to 2198, of SEQ ID NO:43.

43. (Previously Presented) The vector of claim 41, wherein said polynucleotide sequence is as set forth in SEQ ID NO:43.

44. (Previously Presented) The vector of claim 41, wherein said polynucleotide sequence includes a segment of SEQ ID NO:43, said segment encodes said polypeptide having said heparanase catalytic activity.

45. (Previously Presented) The vector of claim 41, wherein said polypeptide includes an amino acid sequence as set forth in SEQ ID NO:44.

46. (Previously Presented) The vector of claim 41, wherein said polypeptide includes a segment of SEQ ID NO:44 said segment harbors said heparanase catalytic activity.

47. (Previously Presented) The vector of claim 41, wherein said polynucleotide sequence is selected from the group consisting of double stranded DNA, single stranded DNA and RNA.

48. (Previously Presented) The vector of claim 41, wherein said vector is a baculovirus vector.

49-58. (Canceled)

59. (Previously Presented) An isolated polynucleotide fragment comprising a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, wherein said polypeptide shares at least 95% homology with SEQ ID NO:44 as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin, wherein said polypeptide is characterized by being about 50 or about 65 kDa, and said polypeptide is characterized by being capable of being purified with a purification procedure initiated with Heparin-Sepharose chromatography, followed by gel filtration and pooling of active column fractions, wherein a quantity of said polypeptide after said purification correlates with heparanase activity in said pooled active column fractions.